

SEQUENCE LISTING

<110> Issa, Jean-Pierre

<120> CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
METHODS OF USE THEREFOR

<130> JHU1590

<140> 09/398,522
<141> 1999-09-15

<160> 120

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1

5

10

13

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ggc cgg cgg ggg cgg ggg tca gca gaa aag gac cgg ggc agc gcg gac Gly Arg Pro Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp 30 35 40 45	507
tcc gag gcg gag ggg ctg ccg tac ccg gcg ctg gca ccg gtg gtt tcc Ser Glu Ala Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe 50 55 60	555
tcc tac ttg agc cag gag agc cgc cgg agc tgg tgg ttc cgc acc Phe Tyr Leu Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr 65 70 75	603
gtc tgt aac ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc Val Cys Asn Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu 80 85 90	651
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gac tcc caq cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt Asp Ser Gln Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe 110 115 120 125	747
gcc ttc ttt gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc Ala Phe Phe Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile 130 135 140	795
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gtc agc ttc tca gct gtc agg aca gtc cgt gtg ctg cga ccc ctc agg Val Ser Phe Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg 175 180 185	939
gcc att aac cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu 190 195 200 205	987
gat acg ctg ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc gtc Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val 210 215 220	1035
ttc ttc atc ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt Phe Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu 225 230 235	1083
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atc tgc tcc cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg Ile Cys Ser Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val 270 275 280 285	1227
ccc acg ctg cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac Pro Thr Leu Arg Gly Asp Gly Gly Pro Pro Cys Gly Leu Asp 290 295 300	1275
tat gag gcc tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac Tyr Glu Ala Tyr Asn Ser Ser Asn Thr Thr Cys Val Asn Trp Asn 305 310 315	1323
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gtc atc acg ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp 350 355 360 365	1467
gct cat tcc ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val 370 375 380	1515
gga tcc ttc ttc atg atc aac ctg tgc ctg gtg att gcc acg cag Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln 385 390 395	1563
ttc tca gag acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg 400 405 410	1611
gtg cgg ttc ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc Val Arg Phe Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro 415 420 425	1659
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aag gca gcc cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg Lys Ala Ala Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg 450 455 460	1755
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ccc agc agc agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac Pro Ser Ser Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His 480 485 490	1851

15

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Leu Val His His His His His His His His His Tyr His Leu Gly Asn	
495 500 505	
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Gly Thr Leu Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp	
510 515 520 525	
gcc aat ggg tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gac	1995
Ala Asn Gly Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala	
530 535 540	
ctc tcc ggg gcc ccc cat ggt ggc gca gag tct gtg cac agc ttc tac	2043
Leu Ser Gly Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr	
545 550 555	
cat gcc gac tgc cac tta gag cca gtc cgc tgc cag gcg ccc oct ccc	2091
His Ala Asp Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro	
560 565 570	
agg tcc cca tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg	2139
Arg Ser Pro Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val	
575 580 585	
tat ccc acc gtc cac acc agc oct cca ccg gag acg ctg aag gag aag	2187
Tyr Pro Thr Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys	
590 595 600 605	
gca cta gta gag gtc oct gcc agc tct ggg ccc cca acc ctc acc agc	2235
Ala Leu Val Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser	
610 615 620	
ctc aac atc cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag	2283
Leu Asn Ile Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu	
625 630 635	
aca cag agt aca ggt gcc tgc caa agc tct tgc aag atc tcc agc oct	2331
Thr Gln Ser Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro	
640 645 650	
tgc ttg aaa gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac	2379
Cys Leu Lys Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr	
655 660 665	
tgt gcc cgg gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg	2427
Cys Ala Arg Ala Gly Ala Glu Val Glu Leu Ala Asp Arg Glu Met	
670 675 680 685	
cct gac tca gac agc gag gca gtt tat gag ttc aca cag gat gcc cag	2475
Pro Asp Ser Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln	
690 695 700	
cac agc gac ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc	2523
His Ser Asp Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly	
705 710 715	
cca gat gca gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt	2571
Pro Asp Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys	
720 725 730	

16

gac acc tpc cga aag att stg gac aac tac ttt ggc egg gga atc 2619
 Asp Thr Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile
 735 740 745

atg atc gcc atc ctg gtc aac aca ctc aac atg ggc atc gaa tac cac 2667
 Met Ile Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His
 750 755 760 765

gag cag ccc gag gag ctt acc aac gco cta gaa atc aac aac atc gtc 2715
 Glu Gln Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val
 770 775 780

ttc acc aac ctc ttt gac ctg gag atg ctg ctg aag ctg ctt gtg tat 2763
 Phe Thr Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Val Tyr
 785 790 795

ggt ccc ttt ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc 2811
 Gly Pro Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val
 800 805 810

att gtg gtc atc aac gtg tgg gag atc gtg ggc cag cag ggg ggc ggc 2859
 Ile Val Val Ile Ser Val Trp Glu Ile Val Gly Gln Gly Gly Gly
 815 820 825

ctg tcc gtg ctg egg acc ttc ccc ctg atg cgt gtg ctg aag ctg gtg 2907
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cgc ttc ctg ccc gcg ctg cag cgg cag ctg gtg gtc atg aag acc 2955
 Arg Phe Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr
 850 855 860

atg gac aac gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc 3003
 Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe
 865 870 875

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 880 885 890

gag cgg gat ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg 3099
 Glu Arg Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu
 895 900 905

ctc tgg gcc atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg 3147
 Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp
 910 915 920 925

aac aaa gtc ctc tac aat ggt atg gcc tcc aac tcc tgg gcc gco 3195
 Asn Lys Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala
 930 935 940

ctt tat ttc att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat 3243
 Leu Tyr Phe Ile Ala Leu Met Thr Phe Gly Asp Tyr Val Leu Phe Asn
 945 950 955

ttg ctg gtc gcc att ctg gtg gag ggc ttc aag gcg gag gga gat gcc 3291
 Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala
 960 965 970

17

aac aag tcc gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt 3339
 Asn Lys Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly
 975 980 985

gat ggg gac agg aag aag tgc ttg gcc ttg gtt tcc ctg gga gag cac 3387
 Asp Gly Asp Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His
 990 995 1000 1005

ccg gag ctg cgg aag agc ctg ctg ccc act ctc atc atc cac acg gcc 3435
 Pro Glu Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala
 1010 1015 1020

gcc aca ccc atg tcc ctg ccc aag agc acc agc acg ggc ctg ggc gag 3483
 Ala Thr Pro Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu
 1025 1030 1035

gcg ctg ggc cct gcg cgc cgc acc agc agc agc ggg tcg gca gag 3531
 Ala Leu Gly Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu
 1040 1045 1050

cct ggg gcg gcc cac gag atg aag tca ccc ccc agc gca ccc agc tct 3579
 Pro Gly Ala Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser
 1055 1060 1065

ccg cac agc ccc tgg agc gct gca agc agc tgg acc agc agg agc tcc 3627
 Pro His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser
 1070 1075 1080 1085

agc cgg aac agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca 3675
 Ser Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro
 1090 1095 1100

agt gga gag cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag 3723
 Ser Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln
 1105 1110 1115

gat gaa gag gag agc tca gaa gag gaa cgg ggc agc cct gcg ggc agt 3771
 Asp Glu Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser
 1120 1125 1130

gac cat cgc cac agg ggg tcc ctg gag cgg gag ggc aag agt tcc ttt 3819
 Asp His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe
 1135 1140 1145

gac ctg cca gac aca ctg cag gtg cca ggg ctg cat cgc act gac agt 3867
 Asp Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser
 1150 1155 1160 1165

ggc cga ggg tct gct tct gag cac cag gac tcc aat ggc aag tcg gct 3915
 Gly Arg Gly Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala
 1170 1175 1180

tca ggg cgc ctg gcc cgg ccc ctg cgg cct gat gac ccc cca ctg gat 3963
 Ser Gly Arg Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp
 1185 1190 1195

ggg gat gac gcc gat gac gag ggc aac ctg 3993
 Gly Asp Asp Ala Asp Asp Glu Gly Asn Leu
 1200 1205

<210> 52
<211> 1207
<212> PRT
<213> Artificial Sequence

<220>
<223> CACNA1G - a gene encoding a T-type calcium channel

<400> 52
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
1 5 10 15
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Arg Pro
20 25 30
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
100 105 110
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
115 120 125
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
130 135 140
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145 150 155 160
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
165 170 175
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
180 185 190
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
195 200 205
Pro Met Leu Gly Asn Val Leu Leu Cys Phe Phe Val Phe Phe Ile
210 215 220
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225 230 235 240
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
245 250 255
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
260 265 270
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
275 280 285
Arg Gly Asp Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
290 295 300
Tyr Asn Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305 310 315 320
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
325 330 335
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
340 345 350
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
355 360 365
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
370 375 380
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385 390 395 400

19

Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
405 410 415
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
420 425 430
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
435 440 445
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
450 455 460
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465 470 475 480
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
485 490 495
His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
500 505 510
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
515 520 525
Ser Arg Arg Leu Met Leu Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser PRO
565 570 575
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590
Val His Thr Ser Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
645 650 655
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
660 665 670
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
675 680 685
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705 710 715 720
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
725 730 735
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
740 745 750
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
755 760 765
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
770 775 780
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785 790 795 800
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
805 810 815
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Leu Ser Val
820 825 830
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
835 840 845
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
850 855 860
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865 870 875 880

20

Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
 985 890 895
 Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
 900 905 910
 Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
 915 920 925
 Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
 930 935 940
 Ile Ala Leu Met Thr Phe Gly Asp Tyr Val Leu Phe Asn Leu Leu Val
 945 950 955 960
 Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
 965 970 975
 Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
 980 985 990
 Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
 995 1000 1005
 Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
 1010 1015 1020
 Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
 1025 1030 1035 1040
 Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
 1045 1050 1055
 Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
 1060 1065 1070
 Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
 1075 1080 1085
 Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
 1090 1095 1100
 Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
 1105 1110 1115 1120
 Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
 1125 1130 1135
 His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
 1140 1145 1150
 Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
 1155 1160 1165
 Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
 1170 1175 1180
 Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
 1185 1190 1195 1200
 Ala Asp Asp Glu Gly Asn Leu
 1205

<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR (GAPDH)

<400> 53

cggagtcAAC ggatgggtcg tac

23

<210> 54

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

21

<223> primer for PCR (GAPDH)

<400> 54

agcctttctcc atgggtggta agac

24

<210> 55

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 55

aaaaaaacccca aactacaaaaa ac

22

<210> 56

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 56

gttgttggrrg ttgttgrg

18

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> y = C or T

<400> 57

aactatcycc aacyccacaa

20

<210> 58

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 58

aagagatcc ttttttttttt tttxgt

26

22

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 59
aaaatccyaa aaaaaacycc ccc

23

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 60
ggaagtttta ggggrgtagg ggaa

24

<210> 61
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 61
aacyatccct ccctataacc tac

23

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 62
aggtagttatg gtgaggtttg tttt

24

<210> 63
<211> 22
<212> DNA

23

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 63

atcaatactaa aacraaatca aa

22

<210> 64

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 64

aggaaaaagaaa aggttaaggg

19

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 65

aaaaattttaac rcaataaaza aa

22

<210> 66

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 66

tatttgaaga ggtggggaaa

20

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 67

aaactttaac cccacctaac c

21

24

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 68
ggttttgttaat tggatataaay gtt

23

<210> 69
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 69
ccactaactc aaaaactaaaa aa

22

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 70
gggaggtgtaa aaaggatgaa a

21

<210> 71
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 71
ctaacactaa aataaaaaata aa

22

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

25

<400> 72
gtaggatgtt ataygaagag

<210> 73
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

20

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 73
aaacrctaac raacatacta c

21

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 74
gggttttttt tagggattt

20

<210> 75
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 75
gaattaaatt tcaaaaaaac cr

22

<210> 76
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 76
tttaggagga tgyggagtt

19

<210> 77

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer
<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 77
aaaaaaccta acraaacact ta

22

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 78
gttattgtgt agtggagttt gg

22

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 79
actccratta acaaaccAAC

20

<210> 80
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 80
aatatggttt yggttggtaa

20

<210> 81
<211> 19
<212> DNA
<213> Artificial Sequence

27

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 81
tcccttaatt ccacacatt

19

<210> 82
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 82
gttaagggtta gttgggtgtt tta

23

<210> 83
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 83
ctctctacta ccraattctt ct

22

<210> 84
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 84
gtttttggttt tggtttgt

18

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 85
ccactaccaa acaaatcccc

20

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

28

<223> Target sequence for bisulfite-PCR primer

<400> 86

tttattgggg aattttcggg

19

<210> 87

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 87

aacaaaaataa ctactacccc rbc

23

<210> 88

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<400> 88

gtaaaagttagg ggggtgggtgat g

21

<210> 89

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 89

ctccaaaaaaa ctataaatac ccraa

25

<210> 90

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> y = C or T

<400> 90

gagtgagtgaa aggyggtaga tt

22

29

<210> 91
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 91
aacctcacat taacrcteet aaa

23

<210> 92
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 92
gttttttaa gatbgggttt tttag

26

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 93
caaaceccaa acatccctta tcca

24

<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 94
ggattttaggg gtaaggggag gg

22

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

30

<400> 95
aaaaaccaca actaaaaatcc ratt

24

<210> 96
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 96
agtgaggggat ttagtttgtgg ttttg

24

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 97
aactatccrcc aacccacaa

20

<210> 98
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 98
aagagatttt tttttttttt ttttgtt

26

<210> 99
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 99
aaaaatccraa aaaaaacccccc ccc

23

31

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 100
ggaagtttta ggggygttagg ggaa

24

<210> 101
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 101
aacaaaatac aactcccaaa caccc

25

<210> 102
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 102
ttagggtttt attttttaat ttggtt

26

<210> 103
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 103
aaaaaaaaatca cratcccccc tc

22

<210> 104
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

32

<221> misc_feature
 <222> (0)...(0)
 <223> Y = C or T
 <400> 104
 ttggaggtat aataaggaga tttygg

26

<210> 105
 <211> 576
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> gene
 <222> (0)...(0)
 <223> APOB CpG ISLAND

<400> 105
 cccggggaggc gcccctttgga ccttttgcata tccctggcgctt ctgcagccct gggcttcata 60
 taaaatgggggt gggggcgccg gcccgccatt cccacccggga cctgcggggc tgagtgcctt 120
 ttcgggttgc tgccgcgtgag gggccggccc agccagccag ggccgcgcagg ccgaggccag 180
 gcccgcggccc aggagccgcg cccacccgca gggccggggc tgccgcgtgag cccggcgctgc 240
 tggcgctgccg tgccgcgtgctg ctgcgtgtgc tgccgcggccg caggccgggt gaggccgcgg 300
 ccgcgtctgcg ggcgcggccg gggccggggcgg ggagccggccg gaccgcgggtt ggccggggca 360
 gcccggggcctt agggccaggagg gggggccggcc acagggttcca gggccggatgggg 420
 ccagctggcg gcccctgcgcg gtcaggatgt gggggccggccg gatggaggagggg ctggaggagg 480
 ggttccggga gctgcctcc ctccctgaaag gtgaaacctg tgccgggtgtt cccctgtcg 540
 ggcccccttagc accegcgtggg aagacgtggg aagctc 576

<210> 106
 <211> 2093
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> gene
 <222> (0)...(0)
 <223> CACNA1G CpG ISLAND

<400> 106
 cctggggccc taaggccaggaa ccccgccgg aataactctga ttcttcgggc tccctccaag 60
 ggagtcccaa agacccaaat ggcataatagg aaagtgggtt cggctctgggc aqcgatctga 120
 ttggctccaaat ctttcggggat cggacccagg ggcaaggggg gggggagaggg ggggttcctgg 180
 gttttggggat gggaaatcgga ttccatgtgtt gtttcttcctc ctgcgttccccc gcccgccactg 240
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 gtcgtggccgc cggccacccgg taaggccaggc gtcgttcggcc gggccggccg gggggccggca 480
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33

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ccctgggggt	tggaggcaca	acaaggagat	tccggccggcg	gtgtatgtca	ggggcgcaga	1980
atgagaacaa	gtgtgggtgg	agggggagctg	tctgcccccc	gagctggggag	tggagccct	2040
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<210> 107

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> CDX2 CpG Island

<400> 107

ctcggttaatc	acggaaagccg	ccggccctggg	gttcggccacg	ccagccctgtg	cggttcttcc	60
ccggccctgtc	agccctgtgg	gaaggagggtg	ggaggaaaaga	aggaagaaaag	ggagggagg	120
aggaggcagg	ccagagggg	ggacccctc	ggaggccagaa	gagccgcag	gagccagogg	180
agcacccggg	gttggggcgc	agccaccccg	cgccctctcg	gtcccccctcg	ccctttccct	240
tctgtcccccc	ccggccctc	cagegtcggt	ccccaggccag	catggtgagg	tctgtccccc	300
gtccctcgcc	accatgtacg	tgagctta				327

<210> 108

<211> 1663

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> EGFR CpG Island

<400> 108

gtcccgccggg	acccgggtcca	gagggggcagt	gttgggaacg	ccctctctgg	aaattraactc	60
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ggggccaccg	tgtccaccgc	ctcgccggcg	ctggccctgg	gtccccctgt	ctgggttctcc	180
tccctctcc	tcgtatctt	ctccctctt	gtccctcccg	atccctcttc	cgccgcctgg	240
tccctctcc	tcccgccctg	ctcccccggc	ctccggcccg	gcgagctaga	ctgtccggca	300
cccccccgcc	cagcgccggc	gcagcagcc	ctcccccctcg	caeggtgtga	gagcccccgg	360
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cacggccccc	cgactccgtc	cagtattgt	ccggagagcc	ggagcgagct	cttggggggag	540
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gcggggcgag	tccgggtctg	gaggaaaaga	aaggtaaggg	cggtatcg	gtcccccggc	660
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agacccgggc	tccggccag	gccccgggaa	ccctccggccgc			900

34

cccgaaacccgt	cccccaacttt	cttccctcaac	tttcccccggcc	cagctgcgcac	ggatcggcgt	960
cagtggccgt	aaggccgggt	ctgggtgggg	cctggggccgg	gggtccccgcac	gggggtcccc	1020
ggcgctgttt	cccaggccgc	gacgggggttt	ttggcgccac	ccgaggggccgg	ctgcggccaccc	1080
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cgccgcgaaa	gcccccaaggt	ctcccttcgtat	ggccggccgt	ccggagacgtc	cggggtctgt	1560
ccacctgcag	cccttcgggtc	gcccgtgggg	ttccgggttgg	agccgggacgc	gggtgttgg	1620
ccactgcagg	gggggatccgc	ggggacttttgc	agggaaaccc	ccg		1663

<210> 109

<211> 1787

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> FBN1 CpG Island

<221> misc_feature

<222> (1)...(1787)

<223> n = A,T,C or G

<400> 109

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cctcggttgg	cacagcgttttt	tctggcgccgg	ccccgggttt	cgaaaggccccc	agtctttttcc	120
tcctggccctt	gggggttttttgc	tgatgtgttt	gggggggggg	ccgggggggg	ggcttacccgg	180
gagggcgggg	caggggggac	tgggtttttt	ccccgggggg	ggcttccgggg	caacgttctc	240
caggccgtat	tcttgcgttt	gggtttttttt	ccccgggggg	ccgtttaggggt	tccatctatcc	300
ccccgggggt	taatcttgcgt	ttttttttttt	ccccgggggg	ccgggggttttt	tttttttttttt	360
ccaccccttcc	ccatccatcc	ccccccccc	ttttttttttt	ccgggggttttt	aaaaaaatgtt	420
cctgtatcc	tctgtttttt	ccccccgttt	ttttttttttt	ccgggggttttt	tttttttttttt	480
ggccgggggt	gttttttttttt	ttttttttttt	ttttttttttt	ccgggggttttt	tttttttttttt	540
gtttttttttt	tttttttttttt	ttttttttttt	ttttttttttt	ccgggggttttt	tttttttttttt	600
ttttttttttt	tttttttttttt	ttttttttttt	ttttttttttt	ccgggggttttt	tttttttttttt	660
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ttttttttttt	tttttttttttt	ttttttttttt	ttttttttttt	ccgggggttttt	tttttttttttt	900
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<210> 110
<211> 810
<212> DNA
<213> *Homo sapiens*

<220>
<221> gene
<222> (0)...(0)
<223> GPR37 CpG Island

<400> 110

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tggggaaatta	acctgtcccg	ccatcccta	gcctcgagcc	gcgcaggctc	cgccctccg	120
cccttgttcc	ctcccaagctc	ctcccgagtgg	aagccqctac	aatgggttg	aatgaaacgt	180
gtgtgggtt	agtgagtgg	gaaccaccaq	gggatcccgt	ctcccccaca	accagtatct	240
ctcccgaggag	gaggcgaagg	agtgggagga	ggcaacgagc	cgagagtg	gttccgggg	300
cgcgccgac	ggctggagcg	cgggggcgag	gcggggccac	ctccccccttc	cgggccgccc	360
ctgcgttgc	cgcgcggtt	coaggcccca	ccctttccgt	ccggggttg	cccgatgtgg	420
cagtgtactag	ctcccgccg	tagccggca	gtccaccgac	gagggccccc	cttttctccc	480
ccctttccccc	acgatttct	tctctgcgc	ggcacccgc	ccagccgt	gttccccc	540
gttgtcaact	tttggatgg	ggagaagcaa	ctttggcagt	ggccgggggg	ttggaaatccc	600
gtttttccctc	ggcagcagta	ggctcgcaag	tgcgtgggtt	taggtggggc	aagagtttcg	660
ccggcgccatc	agcgctgtt	ggggactgttt	gcaacgtgtt	tccagcgagc	ttggagccgg	720
gttgtactg	cgagctgtt	ggggggagggg	gacttttttt	tcttttccctc	tagagaccc	780
ggcttgcac	tggatcaa	acgtgtcgaa				810

<210> 111
<211> 550
<212> DNA
<213> *Homo sapiens*

<220>
<221> gene
<222> (0)...(0)
<223> RSPAA6 CpG Island

<400> 111

tgtattcgca	tggtaacata	tcttgggtct	tcctggcgct	gggtcttcag	cgggccctcca	60
aggcagcccg	caggccccgt	ctcgcttcag	ggatcttcca	cagccccggg	gagacattgc	120
ctctaaagtt	gtcttttttg	cagctctgcc	acaaccggc	gttctcagag	ccagccggga	180
ggagctagaa	cctttccccgc	gttttttca	gcagccctga	gtcagaggcg	ggctggccctt	240
gcaaatgtcc	gccccggcctt	cttcgggtctt	acggacccgt	ccggccggaaac	ttttttccgg	300
ggtcagcggcc	gccccggcgc	ccccgggtctga	cttcggccgg	gggggggggg	gggaggtct	360
cgacttggggc	ggaagggtgcg	ggaagggttcg	cgccgggggg	gtccccgggg	tgcaaaaaggga	420
tggaaaaggccc	gtggacggag	ctggacagat	ccggccgggc	tgccggccaga	gaaacccgcag	480
ggagagccctc	actgtgtgac	ccccctcgac	ggggggggca	gcagccctcg	ttggcccttcag	540
catcccgacaa						550

<210> 112
<211> 278
<212> DNA
<213> *Homo sapiens*

<220>
<221> gene
<222> (0)...(0)
<223> IQGAP2 CpG island

<400> 112

agagttcact tttagttcaag tgtcaagcgcg cggcgccgt ggctggatct ggcgagagag 60

36

caccgaggga	gtgggtcgca	gatotttgggg	gggttagggg	aaatcgccga	gaggcgggat	120
ccgaqcgccg	ggcggggggg	caagacccgg	gagccctggcc	agcgagggtt	gcccgggggg	180
gcgcgccccg	ggcgggcccc	cgagacccgg	caggatcgca	caagaaagac	tgcgtcgat	240
gcagagaccc	cgatcgatgg	ctattgttgg	cgatgaaa			278

<210> 113

<211> 1461

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> KL CpG Island

<400> 113

ctcgaaaagag	ggggcgccgggt	ggggcgccgtt	cccccgccgg	atcttacccaa	aggggggaaatc	60
ccttttccatcg	ccatcgcaag	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	120
tcggcccgatc	ccatatttgc	ttccatgttttt	ttccatgttttt	ttccatgttttt	ttccatgttttt	180
ggggagaaaaag	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	240
ccccccccccaa	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	300
gttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	tttttttttttt	360
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<210> 114

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> PAR2 CpG Island

<400> 114

ccccggggcg	ggccctccgc	agggtggatc	gttgcgttcc	agggtttttt	aaaacccaaac	60
ccgccttgg	ggggcgccca	gcagagggtt	cgatcggtgg	cggtggatgg	gtgtactttt	120
tctcggtgg	ttccatgtgg	tttttttttt	tttttttttt	tttttttttt	tttttttttt	180
ccggcgctgg	ggcttccagg	aggatcggtt	ggcccgccgg	ggccggggat	ccccggcgcc	240
ccatccatcg	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	249

<210> 115

<211> 709
<212> DNA
<213> *Homo sapiens*

<220>
<221> gene
<222> (0)...(0)
<223> PITX2 CpG Island

<400> 115

atgtccgtgtat	cctgtcttcgttcc	ggtttgggttcc	taagtgtcccc	gcctagggttcc	ctatcccttc	60
gtttttccgg	ctccgggttcc	cgacttttcc	gccccgttggc	atctgttcc	ctccctgttcc	120
tctgttttctcg	tcggcccttgc	tctgtttttttcc	cggttgttgc	ccgggggttgc	tgttgttgc	180
tggatcgcca	ggccggcgac	gggggttggc	ggggcccccgg	cgccggacttgc	tgcagtggag	240
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agagaggggat	gagaggggggg	gagaggagag	aqagtgtggag	accggagcgag	aaagctggag	360
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cttccttcgg	actttggca	cttggggatcc	ctgttgttcc	cttggggccgg	gtttttttgggc	480
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ctgtgttgcgg	cgtgttgc	atttagagaaa	gataaaaaggcc	agcagggggaa	aatgaggac	660
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<210> 116

<211> 1496

<212> DNA

<213> *Homo sapiens*

220

<221> gene

<222> (0) ... (0)

<223> PTCA CpG Island

<221> misc_feature

<222> (1) . . . (1496)

<223> n = A, T, C or G

<400> 116

ggggccgcacg	cgcgacgacgc	gcccccccggt	ttagcageag	cagcggctgg	tctgtcaacc	60
ggagcccgag	cccgacgacgc	ctggggccag	cagcttcetc	gcaagccgag	cgccccagggcg	120
cgccaggagc	ccgacgacgc	ggcagcageg	cggccggccg	cccgaaagc	ctccgtcccc	180
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gactntntn	ttcccaacttt	nttttccct	acctntaact	ctnnggggat	cgccccggcc	480
acacacaac	acacacactn	ttttccctttn	tnttccacac	acaacacaca	cactcactca	540
caacttctnca	ggaaaaggcg	cacacaaaatg	gggattgtaaa	aattccaaacc	ctccctctgg	600
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38

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<210> 117
<211> 701
<212> DNA
<213> *Homo sapiens*

<220>
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<222> (0)...(0)
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<221> misc_feature
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<223> n = A,T,C or G

54002 117

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<210> 118
<211> 273
<212> DNA
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<220>
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<400> 118

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<210> 119

<211> 751

<212> DNA

<213> *Homo sapiens*

<220>

<221> gene

<222> (0) . . . (0)

<223> SDC4 CpG Island

<400> 119

39

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<210> 120

<211> 673

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA fragment termed MINT31

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<223> n = A,T,C or G

<400> 120

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